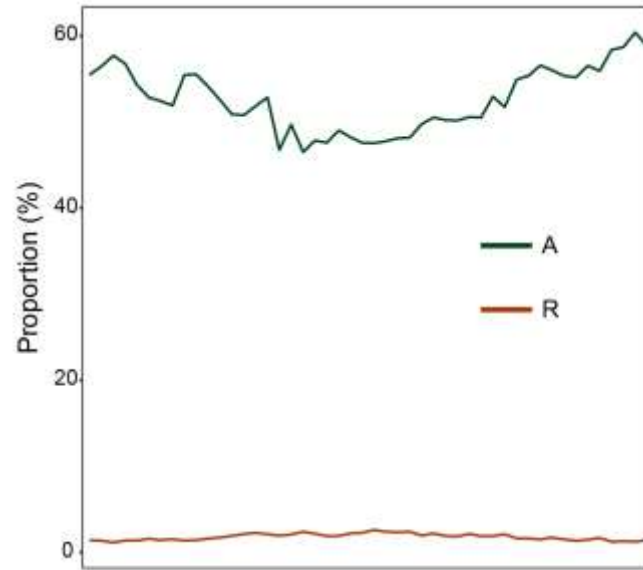
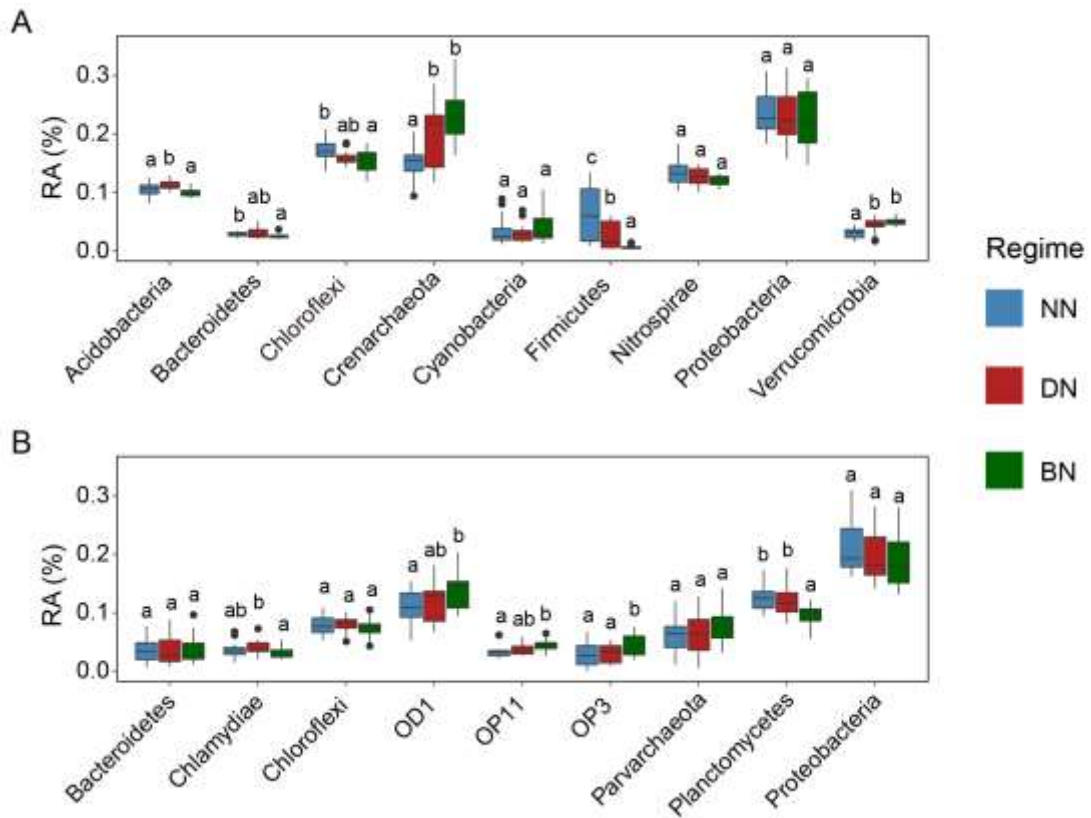


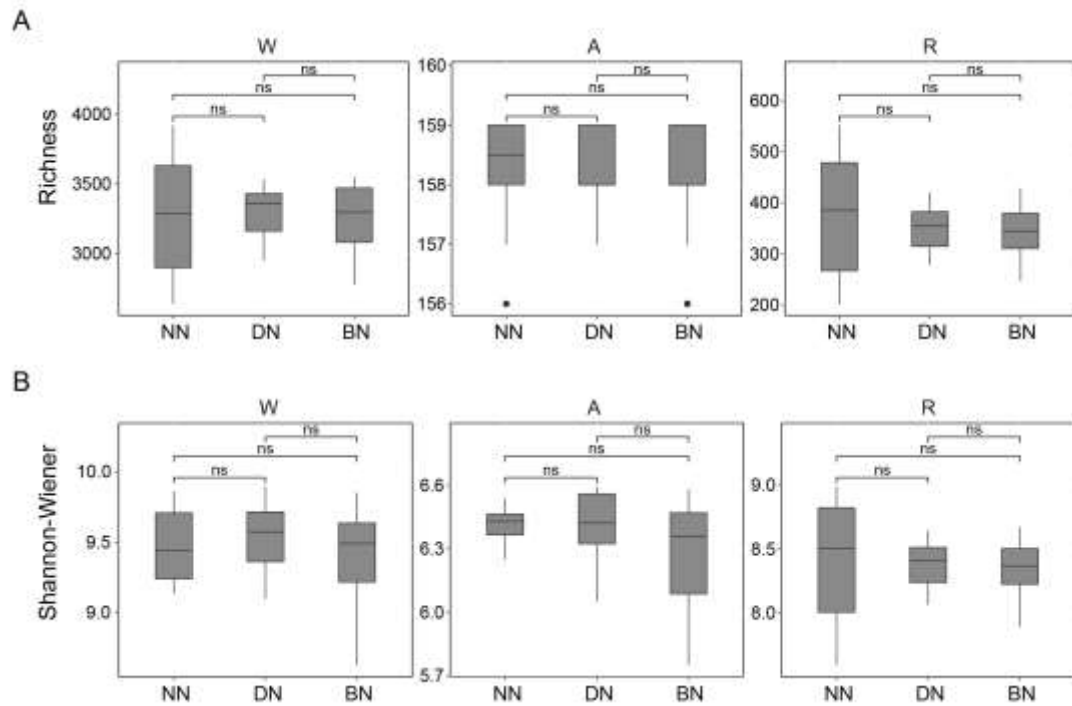
Appendix A Rarefaction curves of detected bacterial species of the rhizosphere microbiota reach the saturation stage with increasing numbers of sequences, indicating that the rhizosphere microbiota in this study capture most rhizosphere bacteria members from each rhizosphere samples. Each colored line represents an single sample. BN, broadcast of N fertilizer treatment; DN, N deep placement; NN, no N fertilizer treatment; Tilling, tillering stage; Jointing, jointing stage; Yellow ripeness, yellow ripeness stage; Harvest, harvest stage.



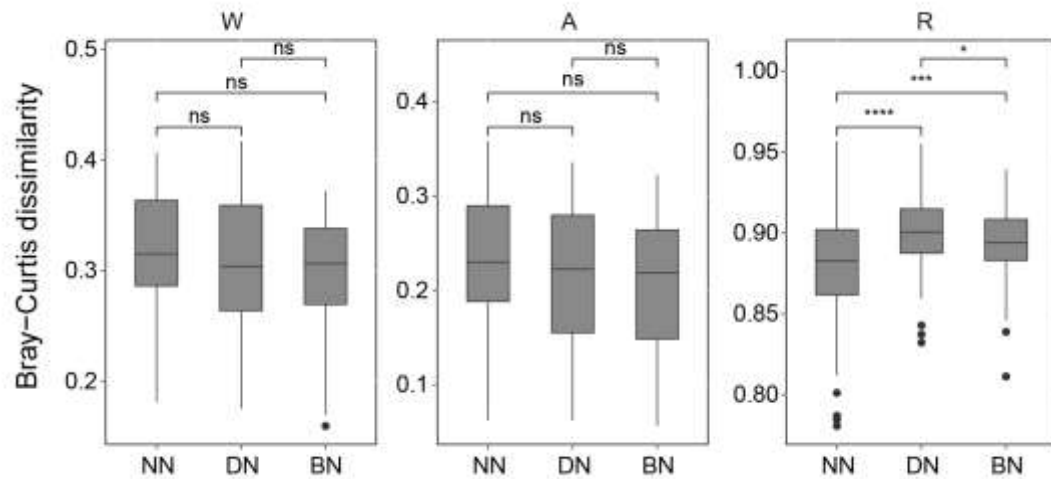
Appendix B The relative abundance of abundant and rare taxa, compared to the whole bacterial community in each sample. A, abundant taxa; R, rare taxa.



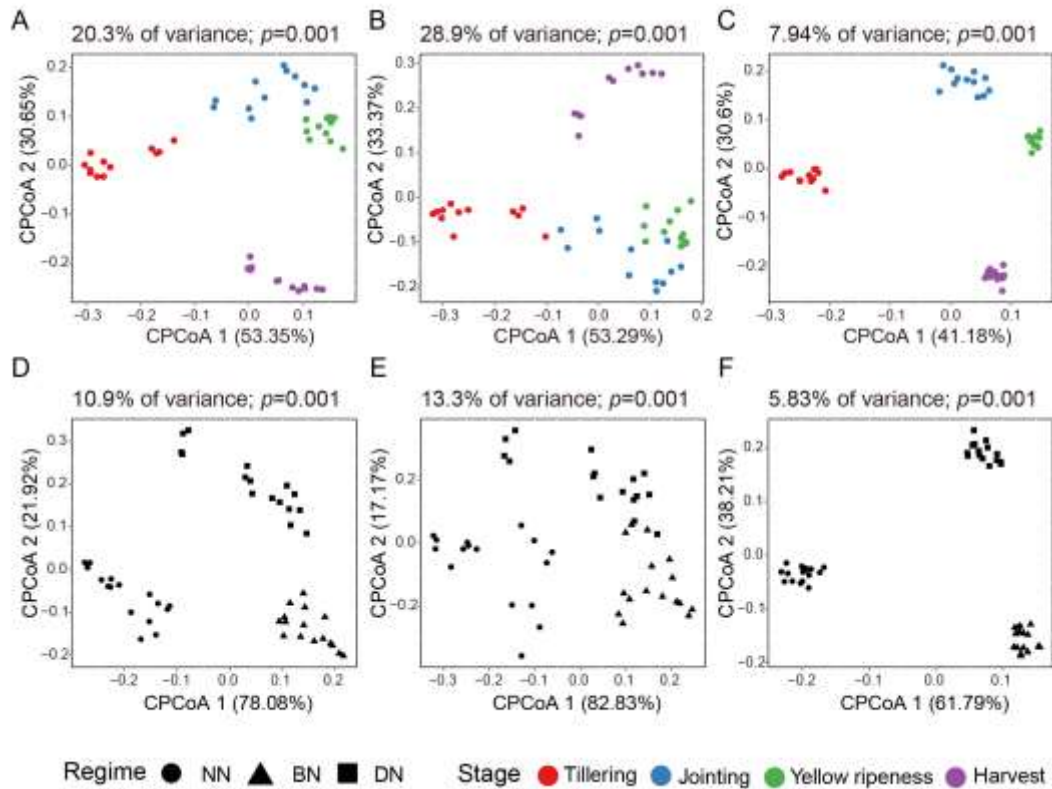
Appendix C Relative abundances (RA) in dominant phyla of the abundant taxa and rare taxa in different fertilization regime samples. A, relative abundances in dominant phyla of the abundant taxa. B, relative abundances in dominant phyla of the rare taxa. Different lowercase letters indicate significant differences ($P < 0.05$; multiple comparison with Kruskal-Wallis tests). BN, broadcast of N fertilizer treatment; DN, N deep placement; NN, no N fertilizer treatment.



Appendix D Richness index and Shannon-Wiener index of different bacterial communities under three fertilization regimes. A, Richness index of the whole, abundant, and rare bacterial communities. B, Shannon-Wiener index of the whole, abundant, and rare bacterial communities. All indices were significantly different between different fertilization regimes determined by Wilcoxon rank sum tests (ns, no significance). W, whole bacterial communities; A, abundant taxa; R, rare taxa. BN: broadcast of N fertilizer treatment; DN: N deep placement; NN: no N fertilizer treatment.



Appendix E Difference in β -diversity among different fertilization regimes of the whole, abundant, and rare taxa (****, $P < 0.0001$; ***, $P < 0.001$; *, $P < 0.05$; ns, no significance; Wilcoxon rank-sum test). W, whole bacterial communities; A, abundant taxa; R, rare taxa. BN, broadcast of N fertilizer treatment; DN, N deep placement; NN, no N fertilizer treatment.



Appendix F CAP analysis of different bacterial sub-communities. A, CAP analysis constrained to fertilization regime for the whole sub-community. B, CAP analysis constrained to fertilization regime for the abundant sub-community. C, CAP analysis constrained to fertilization regime for the rare sub-community. D, CAP analysis constrained to growth stage for the whole sub-community. E, CAP analysis constrained to growth stage for the abundant sub-community. F, CAP analysis constrained to growth stage for the rare sub-community. All variances attributable to the constrained factor and the significance of the factor are portrayed in each plot. BN, broadcast of N fertilizer treatment; DN, N deep placement; NN, no N fertilizer treatment; Tillering, tillering stage; Jointing, jointing stage; Yellow ripeness, yellow ripeness stage; Harvest, harvest stage.

Appendix G The mapping of five ecological processes influencing community turnover within regime varieties.

Taxa ¹⁾	Ecological process	Variable selection (%)	Homogeneous Selection (%)	Dispersal limitation (%)	Homogenizing Dispersal (%)	Undominated Process (%)
A	NN	0	0	7.5	0	92.5
	DN	0	0	11.67	0	88.33
	BN	0	0	10.83	0	89.17
R	NN	0.84	5.83	1.67	15.83	75.83
	DN	0	6.67	16.67	5	71.66
	BN	0.83	1.67	5.83	5.83	85.84

¹⁾A, abundant taxa; R, rare taxa; BN, broadcast of N fertilizer treatment; DN, N deep placement;

NN, no N fertilizer treatment.

Appendix H Lists of keystone species in co-occurrence network.

OTU ID	Degree	Betweenness centrality	Taxa ¹⁾	Taxonomy
OTU_5118	23	3866.449687	A	Crenarchaeota MCG pGrfC26 Unidentified
OTU_140	30	3142.977182	A	Euryarchaeota Methanobacteria Methanobact eriales Methanobacteriaceae
OTU_3391	23	4133.088496	A	Chloroflexi Anaerolineae envOPS12 Unidenti fied
OTU_3985	34	2660.20295	A	Chloroflexi Anaerolineae envOPS12 Unidenti fied
OTU_5994	49	3033.167929	R	Proteobacteria Betaproteobacteria Burkholder iales Burkholderiaceae
OTU_335	46	4278.000334	A	Proteobacteria Deltaproteobacteria Desulfuro monadales Geobacteraceae
OTU_5136	37	4160.56386	R	Bacteroidetes Bacteroidia Bacteroidales GZK B119
OTU_34	30	115.9538682	A	Proteobacteria Betaproteobacteria Burkholder iales Alcaligenaceae
OTU_4312	41	4203.455395	R	Thermi Deinococci Deinococcales Deinococc aceae
OTU_5788	26	388.3235132	R	Planctomycetes Phycisphaerae WD2101 Unid entified
OTU_4338	44	4335.206379	R	Proteobacteria Betaproteobacteria Rhodocycl ales Rhodocyclaceae
OTU_5573	43	4657.099164	R	Bacteroidetes Bacteroidia Bacteroidales Unid entified
OTU_4894	27	1953.611789	R	Planctomycetes Phycisphaerae WD2101 Unid entified
OTU_7226	23	3267.280972	R	Planctomycetes Planctomycetia Pirellulales Pi rellulaceae
OTU_8617	27	1168.641355	R	Proteobacteria Unidentified Unidentified Uni dentified
OTU_8013	31	4419.366623	R	Firmicutes Clostridia Clostridiales Clostridiac eae
OTU_6025	63	3771.32456	R	Chlamydiae Chlamydiia Chlamydiales Parach lamydiaceae

Appendix H Continued

OTU ID	Degree	Betweenness centrality	Taxa	Taxonomy
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OTU_7054	27	2283.743539	R	Proteobacteria Alphaproteobacteria Rickettsiales mitochondria
OTU_3480	59	4292.494019	R	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
OTU_8361	37	2948.419477	R	Proteobacteria Alphaproteobacteria Rickettsiales mitochondria
OTU_3164	25	313.5650126	R	Proteobacteria Alphaproteobacteria Rhodospirillales Acetobacteraceae
OTU_5872	22	3563.226934	R	Unidentified Unidentified Unidentified Unidentified
OTU_5318	27	4598.756373	R	Cyanobacteria Synechococcophycidae Pseudanabaenales Pseudanabaenaceae
OTU_5425	31	654.6792909	R	Proteobacteria Gammaproteobacteria Pseudomonadales Moraxellaceae
OTU_4123	40	2590.546515	R	Unidentified Unidentified Unidentified Unidentified
OTU_6224	25	2354.409917	R	GN02 GKS2-174 Unidentified Unidentified
OTU_6067	45	4100.79945	R	OD1 ZB2 Unidentified Unidentified
OTU_4222	35	1295.401117	R	Cyanobacteria Nostocophycidae Stigonematales Rivulariaceae
OTU_8508	23	1183.718013	R	TM6 SJA-4 Unidentified Unidentified
OTU_2848	36	4270.478721	R	Parvarchaeota Parvarchaea WCHD3-30 Unidentified
OTU_8063	42	3753.74652	R	Proteobacteria Deltaproteobacteria Unidentified Unidentified
OTU_4230	28	2279.574579	R	Firmicutes Clostridia Clostridiales Clostridiaceae
OTU_5427	30	4106.770315	R	TM6 SBRH58 Unidentified Unidentified
OTU_8003	21	1504.101502	R	Bacteroidetes Sphingobacteriia Sphingobacteriales Unidentified
OTU_5087	23	4319.235703	R	Actinobacteria MB-A2-108 0319-7L14 Unidentified
OTU_5277	43	3532.355525	R	OD1 ZB2 Unidentified Unidentified
OTU_4183	30	3986.423227	R	Elusimicrobia Elusimicrobia 0.74 Unidentified

Appendix H Continued

OTU ID	Degree	Betweenness centrality	Taxa	Taxonomy
OTU_4949	25	4074.731844	R	Verrucomicrobia Opitutae Unidentified Unidentified

OTU_7227	32	3948.568246	R	OD1 ZB2 Unidentified Unidentified
OTU_4262	27	2457.618252	R	Planctomycetes Phycisphaerae S-70 Unidentified
OTU_8313	40	729.505634	R	Parvarchaeota Parvarchaea YLA114 Unidentified
OTU_6812	33	607.5562208	R	Parvarchaeota Parvarchaea WCHD3-30 Unidentified
OTU_7636	31	3479.868333	R	WS2 SHA-109 Unidentified Unidentified
OTU_4950	25	2547.974063	R	Planctomycetes Phycisphaerae Phycisphaerales Unidentified
OTU_5157	22	3885.323535	R	Lentisphaerae Lentisphaeria Lentisphaerales 0.66
OTU_5562	27	805.3309748	R	Proteobacteria Deltaproteobacteria 0.83 Unidentified
OTU_8398	29	2479.257661	R	OD1 ABY1 Unidentified Unidentified
OTU_6255	23	2131.836721	R	Verrucomicrobia Pedosphaerae Pedosphaerales Unidentified
OTU_5889	28	2590.678012	R	Planctomycetes Phycisphaerae WD2101 Unidentified
OTU_7186	22	1411.009229	R	Proteobacteria Alphaproteobacteria Rickettsiales Unidentified
OTU_6214	22	1754.547523	R	Parvarchaeota Parvarchaea YLA114 Unidentified
OTU_6729	21	2432.675529	R	Elusimicrobia Elusimicrobia Elusimicrobiales Unidentified
OTU_4571	36	2121.109426	R	Parvarchaeota Parvarchaea WCHD3-30 Unidentified
OTU_4964	21	1125.056775	R	Actinobacteria Acidimicrobia Acidimicrobiales Unidentified
OTU_8164	36	4780.382623	R	Bacteroidetes Saprospirae Saprospirales Chitinophagaceae
OTU_8201	26	1705.488357	R	Proteobacteria Gammaproteobacteria Chromatiales Chromatiaceae
OTU_5627	22	627.4741676	R	Proteobacteria Alphaproteobacteria Rhizobiales Unidentified
OTU_2508	30	3887.420326	R	Proteobacteria Alphaproteobacteria Rickettsiales Unidentified
OTU_8399	29	656.1971488	R	OD1 Unidentified Unidentified Unidentified

Appendix H Continued

OTU ID	Degree	Betweenness centrality	Taxa	Taxonomy
OTU_3855	32	2164.001109	R	Chloroflexi Anaerolineae SBR1031 SJA-101
OTU_6447	33	3128.015949	R	Planctomycetes Planctomycetia Gemmatales

				Gemmataceae
OTU_7337	25	4483.607235	R	Parvarchaeota Parvarchaea YLA114 Unidentified
OTU_4589	36	4871.33985	R	Proteobacteria Deltaproteobacteria Myxococcales Unidentified
OTU_5481	26	2025.216535	R	Proteobacteria Gammaproteobacteria Legionellales Coxiellaceae
OTU_5651	23	4312.6783	R	Planctomycetes Brocadiaceae Brocadiaceae Brocadiaceae
OTU_6947	35	4336.766171	R	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales Verrucomicrobiaceae
OTU_7468	24	2535.742602	R	Acidobacteria Solibacteres Solibacterales Unidentified
OTU_6478	23	113.8519781	R	Firmicutes Clostridia Unidentified Unidentified
OTU_7317	25	567.334244	R	Chlamydiae Chlamydia Chlamydiales 1
OTU_5209	24	4208.145975	R	Bacteroidetes Bacteroidia Bacteroidales Unidentified
OTU_5551	21	4993.636777	R	OD1 ZB2 Unidentified Unidentified
OTU_8758	25	3944.434579	R	WS3 PRR-12 GN03 Unidentified
OTU_5211	26	303.3994673	R	OD1 0.52 Unidentified Unidentified
OTU_5282	21	2275.779122	R	Chlorobi BSV26 PK329 Unidentified
OTU_5817	22	1280.249255	R	Planctomycetes Phycisphaerae AKAU3564 Unidentified
OTU_5065	25	395.0911906	R	Unidentified Unidentified Unidentified Unidentified
OTU_4870	21	26.24082417	R	Firmicutes Clostridia Clostridiales Clostridiaceae
OTU_3978	24	2297.647347	R	Verrucomicrobia Pedosphaerae Pedosphaerales Unidentified
OTU_4171	22	763.5011291	R	Proteobacteria Alphaproteobacteria BD7-3 Unidentified

Appendix H Continued

OTU ID	Degree	Betweenness centrality	Taxa	Taxonomy
OTU_3103	21	65.48541935	R	OP11 OP11-1 Unidentified Unidentified
OTU_5097	23	1140.41031	R	OD1 Mb-NB09 Unidentified Unidentified

¹⁾ A, abundant taxa; R, rare taxa.

